

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: HIRANO, TOSHIO
KAISHO, TSUNEYASU
- (ii) TITLE OF INVENTION: MEMBRANE PROTEIN POLYPEPTIDE HAVING PRE-B CELL GROWTH-SUPPORTING ABILITY AND A GENE THEREOF
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
 - (B) STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 - (C) CITY: ARLINGTON
 - (D) STATE: VA
 - (E) COUNTRY: USA
 - (F) ZIP: 22202
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/624,650
 - (B) FILING DATE: 22-MAY-1996
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/JP94/01732
 - (B) FILING DATE: 14-OCT-1994
- (viii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP 5-281622
 - (B) FILING DATE: 15-OCT-1993
- (ix) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: OBLON, NORMAN F.
 - (B) REGISTRATION NUMBER: 24,618
 - (C) REFERENCE/DOCKET NUMBER: 7625-001-0 PCT
- (x) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 703-413-3000
 - (B) TELEFAX: 703-413-2220

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly
1 5 10 15

Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu
20 25 30

Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala
35 40 45

Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
50 55 60

Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
65 70 75 80

Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
85 90 95

Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
100 105 110

Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
115 120 125

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
130 135 140

Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
145 150 155 160

Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
165 170 175

Ala Leu Leu Gln
180

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 996 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGGAATTCA TGGCATCTAC TTCTGTATGAC TATTGCAGAG TGCCCATGGA AGACGGGGAT	60
AAGCGCTGTA AGCTTCTGCT GGGGATAGGA ATTCTGGTGC TCCTGATCAT CGTGATTCTG	120
GGGGTGCCCT TGATTATCTT CACCATCAAG GCCAACAGCG AGGCCTGCCG GGACGGCCTT	180
CGGGCAGTGA TGGAGTGTG CAATGTCACC CATCTCCTGC AACAAAGAGCT GACCGAGGCC	240
CAGAAGGGCT TTCAGGATGT GGAGGCCAG GCCGCCACCT GCAACCACAC TGTGATGGCC	300
CTAATGGCTT CCCTGGATGC AGAGAAGGCC CAAGGACAAA AGAAAGTGGA GGAGCTTGAG	360
GGAGAGATCA CTACATTAAA CCATAAGCTT CAGGACGCGT CTGCAGAGGT GGAGCGACTG	420
AGAAGAGAAA ACCAGGTCTT AAGCGTGAGA ATCGCGGACA AGAAAGTACTA CCCCAGCTCC	480
CAGGACTCCA GCTCCGCTGC GGCGCCCCAG CTGCTGATTG TGCTGCTGGG CCTCAGCGCT	540
CTGCTGCAGT GAGATCCCAG GAAGCTGGCA CATCTTGGAA GGTCCGTCCT GCTCGGCTTT	600
TCGCTTGAAC ATTCCCTTGA TCTCATCAGT TCTGAGCGGG TCATGGGGCA ACACGGTTAG	660
CGGGGAGAGC ACGGGGTAGC CGGAGAAGGG CCTCTGGAGC AGGTCTGGAG GGGCCATGGG	720
GCAGTCCTGG GTGTGGGGAC ACAGTCGGGT TGACCCAGGG CTGTCCTCCCT CCAGAGCCTC	780
CCTCCGGACA ATGAGTCCCC CCTCTTGTCT CCCACCCCTGA GATTGGGCAT GGGGTGCGGT	840
GTGGGGGGCA TGTGCTGCCT GTTGTATGG GTTTTTTTG CGGGGGGGGT TGCTTTTTTC	900
TGGGGTCTTT GAGCTCCAAA AAATAAACAC TTCCCTTGAG GGAGAGCAAA AAAAAAAA	960
AAAAAAAAAA AAAAAAAA AAAGAATTCC ACCACA	996